

Result No.	Score	Query Match	Length	DB ID	Description
1	918	39.6	444	2	139294 McLeod Syndrome as hypothetical prote
2	129	5.6	439	2	T2470 hypothetical prote
3	120.5	5.2	382	2	E75203 hypothetical prote
4	119.5	5.2	745	2	T02024 cytochrome b245 be
5	118.5	5.1	783	2	A96825 hypothetical prote
6	113.5	4.9	508	2	D0567 hypothetical prote
7	112.5	4.9	785	2	B82299 hypothetical prote
8	109.5	4.7	461	2	B73035 probable cation eff
9	109.5	4.7	498	2	T11039 NADH2 dehydrogenas
10	108	4.7	459	2	T11163 NADH2 dehydrogenas
11	107	4.6	459	2	T11166 NADH2 dehydrogenas
12	107	4.6	459	2	T1172 ferric anguibacina
13	106.5	4.6	341	2	G2880 NADH2 dehydrogenas
14	105.5	4.6	459	2	T17169 brain-specific ang
15	105.5	4.6	1584	2	T00026 probable membrane
16	105	4.5	740	2	A01600 probable transport
17	104.5	4.5	741	2	F00739 probable transport
18	104.5	4.5	741	2	H65589 probable membrane
19	104	4.5	786	2	H64817 transmembrane tran
20	103.5	4.5	503	2	D5104 hypothetical prote
21	103.5	4.5	2143	2	G6595 related to SREBP C
22	102.5	4.4	313	2	T121603 NADH2 dehydrogenas
23	102.5	4.4	378	2	T56228 hypothetical prote
24	102.5	4.4	405	2	S33040 probable membrane
25	102.5	4.4	521	2	T15322 hypothetical prote
26	102.5	4.4	1154	2	T48829 related to SREBP C
27	102	4.4	474	2	S63658 NADH2 dehydrogenas
28	101.5	4.4	438	2	T32208 hypothetical prote
29	101	4.4	459	2	T17181 NADH2 dehydrogenas

GenCore version 5.1.4\_D5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.  
  
OM protein - protein search, using bw model  
Run on: April 1, 2003, 08:45:46 ; Search time 47 Seconds  
(without alignment)  
918.391 Million cell updates/sec  
  
Title: US-09-768-781-3  
Perfect score: 2316  
Sequence: 1 MDRVYEIPBEPNPVDPVSSLE.....RTRVENSEPPFETEARQSVV 449  
  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
  
Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

RESULT 1  
139294  
McLeod syndrome-associated protein XK - Human  
N:Alternate names: Probable membrane transport protein  
C:Species: Homo sapiens (man)  
C:Accession: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 01-Dec-2000  
R:Khamlichchi, S.; Bailey, P.; Blanchard, D.; Goossens, D.; Cartron, J.P.; Bertrand, O., R:Ho, M.; Chelly, J.; Carter, N.; Danek, A.; Crocker, P.; Monaco, A.P.  
Cell 77, 869-880, 1994  
A:Title: Isolation of the gene for McLeod syndrome that encodes a novel membrane transpo  
A:Reference number: 54300; MUID: 94273191; PMID: 804674  
A:Accession: I3294  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues 1-44 <RFS>  
A:Cross-references: EMBL:232684; PID:9515872; OMIM:314850  
R:Biochem. 228, 931-934, 1995  
A:Map Position: Xp21.2-Xp21.1  
C:Keywords: phosphoprotein; transmembrane protein  
A:Accession: S69126  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues 7-22 <RKA>  
C:Genetics  
A:Gene: GDB:XK  
A:Cross-references: GDB:120499; OMIM:314850  
A:Map Position: Xp21.2-Xp21.1  
C:Keywords: phosphoprotein; transmembrane protein  
Query Match 39.6%; Score 918; DB 2; Length 444;  
Best Local Similarity 44.3%; Pred. No. 1.4E-68;  
Matches 178; Conservative 80; Mismatches 134; Indels 10; Gaps 4;  
Qy 33 PPESLILFSTPELYCGPAAASALYMVRYRKNSSETYRMTYTFSSFMSSIMVQLTLIFYHDL 92  
Db 3 PPSVSLASPLFVAETTAALSSSTYRSGGDRMMQALTLLFSLPCLVQTLFLFYHDL 62  
Qy 93 AKDKPLSLFPHLILLIGPVIRCLEANKIYLWKEEEQEPVWSLPRRK-MLDGBEVIL 151  
Db 93 SRDRPLVLLHLQQLGLPFRCEVCIY--FQSGNNNEEPVSTIKKROMEKNGLSEBIE 119  
Qy 152 WEVGH5IRTLMHNRVAYKRMNSQIAQKYYDKYKIRGLPLEVLCITWRTLEITSRLILVLFSATLKLKAVP 271  
Db 120 KEVGQAEKGKLTHRAFSRASVIAQFLGSAAQTLQYISMQODATVGRSLMTSLLS 179  
Qy 212 VTYGATLCNMIAIQKYYDKYKIRGLPLEVLCITWRTLEITSRLILVLFSATLKLKAVP 271  
Db 180 IVYGALRCNTLAIIKTYDEVEVKVNRLAVYCFILWRSPELATRVVVLFLTSVLRKTVVV 239  
Qy 272 FLVNLFLITLFPWIKFWRSQAGMNNIEKFNSRVTLYAGINFSCMWSALQ 331



Qy	150 IEWVGHSIRTTLAMRNAYKRM50I-----QFLGSVPOLTYQLYSSLISAEPVPLGRVVL 204	Db	234 --PKRNPCKEYLSKAETLVFFILLIGITIESDYNSVSVAIGIMFPE-----RQGRT 286
Ddb	125 ELWQ---LETLIQDXTMYSQALSYTQSOLSLAGLRKKSSSIRKIS----- 170	Qy	336 DRDLVDK-----RLVENVIVNLVKPFPFGV-----
Ddb	205 MVSFLSVSITYGATLCNMMLAQIKYDDYKIRGPLEVLCITI-----WRTLEITSRLIL 258	Db	287 HRTLJQRLSYSPHEFVLPVYFGYIGFRFSIATLKRFYLGIVIVIVTIAIGRPVIVSAC 346
Qy	171 -----TSLSY-----YFEDNWKRILWL-----ALWIGIMAGLFWMKFMOYRNRTVFD 212	Qy	373 -----KVLL-NY-----CHSLTLAQLIAYLIS-----
Ddb	259 VL-FSATLKLKAVPVLNFELIIFP-----PWKEFWRSGAQMPNNIEKNSRGTLLV 311	Db	347 MYLKTPKRYTWLPLPTLSVKGHVGLLLDSDNTESEKKWTTTIHDMVVAALVITLVLGVYL 406
Qy	213 VMGYCVTTAKGAETTKLNAAITLPLVCRNTITWLSTRARALPFDNNINPHKTIAAI 272	Qy	395 IDEMLFFQ-----YLHPURSLFTHNVYDYLHVCCC 425
Ddb	312 LISVITYLAGINFCSWSALQRLAEDLVDKGQWNQHMGHLHY----SVRLVENTVNVL 366	Db	407 ASFLIKTREREDEFAVEKTSLESHTNEELRLUSC 439
Ddb	273 VVGI-ILHGNHLVCDPRLKSSDKYAPLQYFGEKPKPTFLVKGEVGTGVNWV 331		
RESULT 6			
Qy	367 F-----KFFGVKVLLNYCHSL-----IAQLII-----AYISID 396	Db	D90567 hypothetical protein MYP0_4440 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
Ddb	332 MIAAITFLATRWFRRSLVVKLPRPFDTLGTGFNAFW-YSHHLFTIVIALIVHGECLYLHW 390	C;Species: Mycoplasma pulmonis	C;Species: Mycoplasma pulmonis
Qy	397 FMLLEPQYL 405	C;Accession: D90567	C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
Ddb	391 YRPTTMYL 399	R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Nucleic Acids Res 29, 2145-2153, 2001	R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Nucleic Acids Res 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycopl			
A;Reference number: A99512; MUID:21267165; PMID:11353084			
A;Accession: D90567			
A;Molecule type: DNA			
A;Residues: 1-508 <KTR>			
A;Cross-references: GB:AU445566; PID:914089858; PIDN:CACT3617.1; GSPDB:GN00153			
A;Experimental source: strain UAB CTIP			
C;Genetics:			
A;Gene: MYP0_4440			
A;Genetic code: SGCG			
Query Match Score 4.0%; Best Local Similarity 18.3%; Pred. No. 0.096; Matches 81; Conservative 90; Mismatches 159; Indels 113; Gaps 20			
Query 28 NPFTEPPSFISLFTSTPLYCGERASALYMVYRKN-----SETYRMTYTFSF---FMFS 77			
Db 95 NHRNPIYIILWFSIYIFSG-----IFLFSRNIPAPITPEFVELYIFYIYVIL 147			
Query 78 SIMVOLTFLVHDLAKDKPLSFLMFLILLGPVIRCLEAMIKYLTLMKKEQEPYVSLT 137			
Db 148 EILLYSVWLUYNRRVERDHLEYAKLKVFL-----IVSMLYVYL-SWINSKSO-----IT 197			
Query 138 RKKMJD-----GEEV-----LIEWEYVHSIRTLAMHNAKYKRSNQIQLAPL 178			
Db 198 TDAKLVEEWLPFYQNRIQAFVASSDEBIVGLIREIGYVAYLIL--IFPFFPSLLYS 254			
Query 179 GSPVQLT-----YOLYVSLISAEVPGRVVLMSVSVTYGATLCNMMLAIQIYKD 229			
Db 255 FKPKRKTQSNKNQNLQNLNIVL-----LEIN 303			
Matches 89; Conservative 69; Mismatches 166; Indels 129; Gaps 19;			
Query 73 FPMESSIMVQLTFLVHDL-----AKDKPLSFLMFLILLGPVIRCLEAMIKYLTLM 124			
Db 16 FNPLNTMFQMACILVYFSQQLFYLLKPCGQAGPVQTLAGIVLSPVLLSRPKKEPLQ 75			
Query 125 KKEEBQEPFL-----LTKKKMLDGEVYGHIRSTLAMHNAKYKRSNQIQLAPL 178			
Db 76 KNAADYYSFFSPALRTSFMFPLIGEVLDFH-----MRN-FKKAavitLSSFVV 124			
Query 179 GSVPQQLTYQLYSSLISAEPVPLGRVVLMSVSVTYGATLCNMMLAIQIYKD 235			
Db 125 GLLSPASMLFIPLGSKIEDFTFLVLLVTSATLKLKAVPFLVNLFLIFP-----DWKLNTCEI 178			
Query 236 GPLEVUCITIWRTRBLBTTSRLLILVLSATLKLKAVPFLVNLFLIFP-----PWIKFWS 291			
Db 179 GRITSCALFELTNVLYTIIMAFISGTTILEFLFELATVILINMVLAPWL-----233			
Query 399 -----LLTSFSSL-YIFMSWHLQDILVITIANFLDFYLLLYLVGFAVMLNFFVVFSSFY 452			
Query 406 HPLRSLFTH-----NVDY 419			
Db 453 KSLSLTKTEKKPWTENKKNFEDY 475			
RESULT 7			
292 GAQMNNTEKNSRGTLLVLI-----SVTLYAGINFSCMNLQRLA 335			

A86299 hypothetical protein F309.18 - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: B86399  
 C;Date: 02-Mar-2001 #Sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;  
*Nature* 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.; Li, J.; Li, Y.; Lin, X.-S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-785 <STOP>  
 A;Cross-references: GB:AE005172; NID:94966359; PIDN:AD34690.1; GSDB:GN00141  
 C;Genetics:  
 A;Map position: 1

Query Match 4.9%; Score 112.5; DB 2; Length 785;  
 Best Local Similarity 19.7%; Pred. No. 0.19; Matches 84; Mismatches 172; Indels 107; Gaps 20;

Qy 37 ILFSTPLY-----CGBAAS-----C-----Q-----  
 Db 30 LVFSQPFYLFLPKCGAQPAQILAGIVLSSITIRKHEFLQDOSASYTIFSPFLRT 89

Qy 84 TLIF-YHRDLAKDKPLSFLMHLILGPVIRCLEAMIKYTLWKEKEQEPVSLPDKML 142  
 Db 90 AFVFLIGLEIDD-----FMGRNLKNSIVITLGSLVSIWL-----PFLWFLLRFMQ 138

Qy 143 IDGE-----EVLINEVEGHS-IRTLMHNRAYKRMNSQIQAFGLS 180  
 Db 139 IKDGFDTFLAFLITLSNTAAPVVISLTSRHTSEIGRAIASCSUFLBTNI-----192

Qy 181 VPQLTYQYELISIAEVPLGRVVLAVFSLVSVTGYATLCNMIAQIKYDDYKIRGPLE- 239  
 Db 193 ---PIYTIVLSPISGMNTADPIYSATGVILTNRFLASLPKRPKPEKYLSKAETLAF 249

Qy 240 -VLCITIWTRLE---ITSRLILV--LFSATLK----LKAPEFLVNLFLPPWK 287  
 Db 250 IILLIITALTIESNSTLTVFPIGMMPREGKTYRTLQIORSYDHEFWLPVFGYIG 309

Qy 288 FWRSQGMQNPNEKNSRSVGTFLVVLISVTLYAGINFSC-----WSALQLRLADRD 338  
 Db 310 FRES-----VNSLTKRYHLGLMTGKGLVFLACPSLKLPKQYNTFLSTMVSK- 364

Qy 339 LVDKGONGWHGHLHYSVRLVENVIMVLFKEFGVKVLLNYCHSLIALQLTAYLIS--ID 396  
 Db 365 -----GHIGL--VLLDSDN---LMLMKWTFPTV---HDMMFVAALVIMTLLSGVIT 405

Qy 397 FMLJFFQ--YLHPLRSLSLTHENVVDYLHCVC 425  
 Db 406 SLLRSQEKSFAHKTSLEFDTEELRVLTc 437

RESULT 9  
 T11039  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Chlamydomonas eugametos mitochondrial  
 C;Species: mitochondrial Chlamydomonas eugametos  
 C;Accession: T11039  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Jun-2002  
 R/Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.  
 Plant Mol. Biol. 36, 285-295, 1998  
 A;Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos.  
 A;Reference number: 217244; MUID:98145434; PMID:9484440  
 A;Accession: T11039  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-498 <DEN>  
 A;Cross-references: EMBL:AF008237; NID:92865253; PIDN:G2865257; PIDN: AAC39340.1  
 C;Genetics:  
 A;Genome: mitochondrial  
 A;Note: nad4  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4  
 C;Keywords: membrane-associated complex; mitochondrial; NAD; oxidative phosphorylation;

B97305 probable cation efflux pump (multidrug resistance protein) [imported] - Clostridium acetobutylicum  
 C;Species: Clostridium acetobutylicum  
 C;Accession: B97305  
 C;Date: 14-Sep-2001 #Sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 R/Nolling, J.; Bennett, G.N.; Koornin, E.V.; Smith, D.R.  
*J. Bacteriol.* 183, 4833-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.  
 A;Reference number: A96900; MUID:21359325; PMID:21359325  
 A;Accession: B97305

RESULT 8  
 B97305  
 probable cation efflux pump (multidrug resistance protein) [imported] - Clostridium acetobutylicum  
 C;Species: Clostridium acetobutylicum  
 C;Accession: B97305  
 C;Date: 14-Sep-2001 #Sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 R/Daly, M.J.; Bennett, G.N.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
*J. Bacteriol.* 183, 4833-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.  
 A;Reference number: A96900; MUID:21359325; PMID:21359325  
 A;Accession: B97305

Query Match 4.7%; Score 109.5; DB 2; Length 498;  
 Best Local Similarity 22.1%; Pred. No. 0.2; Matches 64; Conservative 46; Mismatches 89; Indels 91; Gaps 13;

Qy 185 TYQYXSLISAEVPLGRVVLVFSLVSVTYGA-----TLCNMIAQIKYDDYKIRL- 235  
 Db 40 TYCLFVTMV-----VLMWTLYMSI-XDAIGHSLOMMVVIERLHISFGVDSMSLSLT 90

RESULT 10

Qy 236 ---GPLEVLCITIWRLLE-ITSRLILVLFSATLKLKAVPF-----LVTNFFLILFE 283  
 Db 91 LLTTSALFPICMVWTFKGITIETLLEIIVYGAANLYDLGFLYLFSEASLILFLII--- 147  
 Qy 284 PWKEFWRSGAQMPNNIEKNSRV-----GTLVWLISVTLYAG-----INF---- 324  
 Db 148 -----GRSVYGNIEAAKYIVLTYMGGSLILLPLIPVLYAQGGSTSILYLLCNFGSQH 199  
 Qy 325 -SCSALOURLADRLDYLKGCGNWNGLHYSVRLTENVLYLVEKFGVYKVLITYCHSLI 383  
 Db 200 ADAIOSAYYLSEROMI---LGWG-----LTVFAVKIPLMPVHLWL 238  
 Qy 384 -----ALQLIAYLISIDFMLEFFQYLHPLRSLSFTHNVVDYLHCV 424  
 Db 239 PEAHVAAPTAGSVLAVGULLKLGG;GFIREMIPILPSFTASIFPLVCCMC 288

Query Match Score 4.6\*; Score 107; DB 2; Length 459;  
 Best Local Similarity 19.2%; Pred. No. 0.3%; Indels 122; Gaps 19;  
 Matches 80; Conservative 71; Mismatches 143; Indels 122; Gaps 19;

Qy 35 FSILESTFLYCGEAAASALYMYRIYRNSETYRMYTTSFPMSSIMVQLTLFVHDLAK 94  
 Db 118 FYILFETTLIPTLILITRWNQAEIRLNASTYFLFYLT---GSPLPLIMLFLVHNNGS 173

Qy 95 DKPLSLFPMHLLILGPVIRCLEAMIKYLTNLKKEQEPPVYSLTRKMLIDGEVLTIEWV 154  
 Db 174 ---LNT-----PLLTATAQL-----PLLTATAQL-----PLLTATAQL-----  
 Qy 155 GHSHIRTLMERNAKRMSSQIAFLGSPVQPLTYQLYSSLISAEVPL-GRVVLMVFLSLSVT 213  
 Db 191 SHNLTWLAAC-----MFAFMVKMPYGLHLWPKAHVEAPIAGSMVLAALVLLKG 240

Qy 214 YG---ATLGNMMLAOIQKYDDKIRLGPLEVLCITIWRLBITSRLILVLFSATLKLKA 269  
 Db 241 YGMMRLTSILNPITLEMAY-----PPFLMISLWGMINTSSTCLRQDLSLILAYS 290

Qy 270 VPFLVLFNLILFE-PWIKFWRSRGMPPNNIEKNFSRVTLYVLI---SVTLYAGI 322  
 Db 291 VSHMALVIMASLQIOTW-----SFTGAIVLMIAHGLTSMLFCIANS 332

Qy 323 NFSCMSALQRLLADRLDVK-----GONWGHMGLHYSVRL-ENVIMVLVFKPFGV 372  
 Db 333 NYERTHS-RIMLRSGLQTLLPLMAFWAANLTNALPPTINLGBLVMNTSFMSHV 391

Qy 373 KVLLNYCHSLLAJLQLIAYLISIDEFLMFLFO-----YLHPLRSLSFT-HNVYDYLH 421  
 Db 392 TMLT-----GLNMUJIALYSL-YMLVLTQRETLSHINNPKSFRENMIMEMH 440

RESULT 12

Qy 155 GHSHIRTLMERNAKRMSSQIAFLGSPVQPLTYQLYSSLISAEVPL-GRVVLMVFLSLSVT 213  
 Db 191 SHNLTWLAAC-----MFAFMVKMPYGLHLWPKAHVEAPIAGSMVLAALVLLKG 240

Qy 214 YG---ATLGNMMLAOIQKYDDKIRLGPLEVLCITIWRLBITSRLILVLFSATLKLKA 269  
 Db 241 YGMMRLTSILNPITLEMAY-----LMLSLWGMINTSSTLRQDLSLILAYS 290

Qy 270 VPFLVLFNLILFE-PWIKFRSGAQMPNNIEKNFSRVTLYVLI---SVTLYAGI 322  
 Db 291 VSHMALVIMASLQIOTW-----SFTGAIVLMIAHGLTSMLFCIANS 332

Qy 323 NFSCMSALQRLLADRLDVK-----GONWGHMGLHYSVRL-ENVIMVLVFKPFGV 372  
 Db 333 NYERTHS-RIMLRSGLQTLLPLMAFWAANLTNALPPTINLGBLVMNTSFMSHV 391

Qy 373 KVLLNYCHSLLAJLQLIAYLISIDEFLMFLFO-----YLHPLRSLSFT-HNVYDYLH 421  
 Db 392 TMLT-----GLNMUJIALYSL-YMLVLTQRETLSHINNPKSFRENMIMEMH 440

RESULT 11

T17166 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti mi  
 C;Species: mitochondrial Pygathrix bieti  
 C;Accession: T17163  
 R;Wang, W.;Forstner, M.R.J.;Zhang, Y.P.;Lui, Z.M.;Wei, Y.;Huang, H.Q.;Hu, H.G.;X:  
 Int. J. Primatol. 18, 305-320, 1997  
 A;Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences  
 A;Reference number: 218709  
 A;Accession: T17166  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:U92957; NID:92290441; PID:92290444; PIDN:AAD08826.1  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match Score 4.6\*; Score 107; DB 2; Length 459;  
 Best Local Similarity 19.2%; Pred. No. 0.3%; Indels 143; Gaps 122; Gaps 19;

Qy 35 FSILESTFLYCGEAAASALYMYRIYRNSETYRMYTTSFPMSSIMVQLTLFVHDLAK 94  
 Db 118 FYILFETTLIPTLILITRWNQAEIRLNASTYFLFYLT---GSPLPLIMLFLVHNNGS 173

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 03-Jun-2002  
 C;Accession: T17166  
 R;Wang, W.;Forstner, M.R.J.;Zhang, Y.P.;Lui, Z.M.;Wei, Y.;Huang, H.Q.;Hu, H.G.;X:  
 Int. J. Primatol. 18, 305-320, 1997  
 A;Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences  
 A;Reference number: 218709  
 A;Accession: T17163  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:U92956; NID:92290437; PID:92290440; PIDN:AAD08823.1  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match Score 4.7%; Score 108; DB 2; Length 459;  
 Best Local Similarity 19.2%; Pred. No. 0.25%; Indels 122; Gaps 19;  
 Matches 80; Conservative 71; Mismatches 143; Indels 122; Gaps 19;

Qy 35 FSILESTFLYCGEAAASALYMYRIYRNSETYRMYTTSFPMSSIMVQLTLFVHDLAK 94  
 Db 118 FYILFETTLIPTLILITRWNQAEIRLNASTYFLFYLT---GSPLPLIMLFLVHNNGS 173  
 Qy 95 DKPLSLFPMHLLILGPVIRCLEAMIKYLTNLKKEQEPPVYSLTRKMLIDGEVLTIEWV 154  
 Db 174 ---LNT-----PLLTATAQL-----PLLTATAQL-----PLLTATAQL-----  
 Qy 155 GHSHIRTLMERNAKRMSSQIAFLGSPVQPLTYQLYSSLISAEVPL-GRVVLMVFLSLSVT 213  
 Db 191 SHNLTWLAAC-----MFAFMVKMPYGLHLWPKAHVEAPIAGSMVLAALVLLKG 240

Qy 214 YG---ATLGNMMLAOIQKYDDKIRLGPLEVLCITIWRLBITSRLILVLFSATLKLKA 269  
 Db 241 YGMMRLTSILNPITLEMAY-----LMLSLWGMINTSSTLRQDLSLILAYS 290

Qy 270 VPFLVLFNLILFE-PWIKFRSGAQMPNNIEKNFSRVTLYVLI---SVTLYAGI 322  
 Db 291 VSHMALVIMASLQIOTW-----SFTGAIVLMIAHGLTSMLFCIANS 332

Qy 323 NFSCMSALQRLLADRLDVK-----GONWGHMGLHYSVRL-ENVIMVLVFKPFGV 372  
 Db 333 NYERTHS-RIMLRSGLQTLLPLMAFWAANLTNALPPTINLGBLVMNTSFMSHV 391

Qy 373 KVLLNYCHSLLAJLQLIAYLISIDEFLMFLFO-----YLHPLRSLSFT-HNVYDYLH 421  
 Db 392 TMLT-----GLNMUJIALYSL-YMLVLTQRETLSHINNPKSFRENMIMEMH 440

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 03-Jun-2002  
 C;Accession: T17162  
 R;Wang, W.;Forstner, M.R.J.;Zhang, Y.P.;Lui, Z.M.;Wei, Y.;Huang, H.Q.;Hu, H.G.;X:  
 Int. J. Primatol. 18, 305-320, 1997  
 A;Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences  
 A;Reference number: 218709  
 A;Accession: T17162  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:U92959; NID:92290449; PID:92290452; PIDN:AAD08832.1  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match Score 4.6\*; Score 107; DB 2; Length 459;  
 Best Local Similarity 19.2%; Pred. No. 0.3%; Indels 143; Gaps 122; Gaps 19;

Qy 35 FSILESTFLYCGEAAASALYMYRIYRNSETYRMYTTSFPMSSIMVQLTLFVHDLAK 94  
 Db 118 FYILFETTLIPTLILITRWNQAEIRLNASTYFLFYLT---GSPLPLIMLFLVHNNGS 173

C;Species: mitochondrial Pygathrix bieti

Qy	95	DKPLSLPMHLLGVPVIRCLEAMIKYLTWKKKEEQEPPVSLTRKRMIDGEVEVLLIEWEV	154
Db	174	--LNI-----PLTLPQL-----TTW--	190
Qy	155	GHSIRSTLAMHRNAYKRMQSQQAPLGSVQPLTYOLYVSSLSIASEAEPV-GRVYLMVFSLVSVTT	213
Db	191	SHNLTWAC-----MMAPMVKMPYPLHLWPLKHAVEAPIAGSVLAATLKLGG	240
Qy	214	YG----ATLCNMMLAIQKYDDYKIRLGPLEVLCLITWRTLEITSRLLIVLFLSATLKLKA	269
Db	241	YGMMRRLTSILNPTEVMAY-----PEFLMSLWGMIMTSSCTLRQTDLKSLSIAYSS	290
Qy	270	VPFLVNLINFLIIIFP-EPIKFWRSGAQMPNNIEKNEFSEVTLVWLJ-----SFTILYAGI	322
Db	291	VSHMALVIMASLIOTPW-----SFPIGAVLMIANGITSSMELFLCLANS	332
Qy	323	NFSCWSALQLRQLADRLDVK-----GQNGHMGILHYSTRV-ENVIMVLFKFFEVY	372
Db	333	NYERTHS-RIMLJSRGQIOTLLPMAFWFAANLTNLALPFNTNLIGELVMMTSFSWSV	391
Qy	373	KVLLNCHSLLALQLIIAYLISIDEMLIFQ-----YIHPRLSLFT-HNVVDYLH	421
Db	392	TIMLT-----GLNMLITALYSU-YMLVTTORTGLTSHTINMKPSFTRENMLMEMH	440
<b>RESULT 13</b>			
Qy	682880	ferric anguibactin transport system permease protein UUS16 [imported] - Ureaplasma urealyticum	
C;Species:	Ureaplasma urealyticum		
C;Date:	18-Aug-2000	#sequence_revision	20-Aug-2000 #text_change 20-Aug-2000
C;Accession:	GB:AE002880		
R;Glass:	J.T.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.		
R;Submitted to:	GenBank, February 2000		
A;Description:	The complete sequence of Ureaplasma urealyticum: Alternate views of a minor ribosomal RNA gene.		
A;Reference number:	AE2870		
A;Accession:	GB:AE2870		
A;Status:	preliminary		
A;Molecule type:	UUS16		
A;Residues:	1-341 <GLA>		
A;Cross-references:	GB:AE002150; GB:AE022894; NID:96899515; PIDN:AAF30929.1; GSPDB:GN001		
C;Genetics:			
A;Gene:	fatC-3; UUS16		
A;Genetic code:	SGC3		
Query	Match Score	4.6*	Length 341;
Best Local Similarity	22.3%	Pred. No. 0.24;	
Matches	71;	Mismatches	52;
Local Similarity	22.3%	Indels	79;
Conservative		Gaps	19;
Matches			
Qy	37	ILFSTFL--YCGGEASASYLAMYRIVRQN--SETYRMYTTFSSFMFSSINVQLTUJFVHR-	90
Db	65	IFLSGTILGFCA-----YIQLQLTQKRPFDSDT-----SIMGISSVNILGVIIIAFQVD	111
Qy	91	--DLAKDKPISLEMH---LILGPVTCRLEMAMIKYLTWKKKEQEPPVYUSLTKRMQIJD	144
Db	112	FNNFSADK-LSTLEHTBPIIIFTAPIIIC--MLYYFTIC--KEQS-----SFNYKRMUJS	160
Qy	145	GEEV-LIEWEVGHSI-RTLAMERNAYKRMISQTOAFLGSVPQLTYOLYVSLSIAEVPLGRV	202
Db	161	GVTIVPFLSVALGASIAKPNLKPKNAYVS---RYTYSSEIPEQESFFPALVLLIIGL	215
Qy	203	VLMVFSLVS-VTYGATLICMNLAIQKIQYDDYKIRLGPLEVLCLITWRTLEITSRLLILVLF	261
Db	216	VLPNFKKIQTIVSNQDLANQLGINVKTSGLL---LVAICLNGVASYSLNGNLIFIGIM	271
Qy	262	SATIJKLKAAPPVPLVNLILLPEWIKPAREGQMPNNIEKNEF---RVGTAVLVLISVTI	317
Db	272	AGNM-----GTVISNNRFKSAASISGCCSLYMLSPFL	305
Qy	318	LYAGINP-SGVSALQRL	334
Db	306	FIKLNEDSQMVNLAPL	323

A;Gene: GDB:BAII  
A;Cross-references: GDB:9838088 ; OMIM:602682  
A;Map position: 8q24-8q24  
C;Superfamily: thrombospondin type 1 repeat homology <THR3>  
F;400-462/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match Score 1.05.5; DB 2; Length 1584;  
Best Local Similarity 23.0%; Pred. No. 1.7;  
Matches 65; Conservative 38; Mismatches 98; Indels 81; Gaps 12;

Qy 193 ISAEVPLGRVTLMFSALAVSTYGATLGNMLAIQKDYKIRLGPLEVLCTYWRITLE-- 250  
Db 935 LSADANMEKATLPSVTLL-VCCGVSSLTLMVVIVY-----VSVWYVIRSE 979

Qy 251 ---TTSRLLILY-----LFSATLKLKAVPELVNLNFELAIIIFEPWI 286  
Db 980 RSVLILNFCLSIISSSVALIILIGQTQPRNKVNTLVAAFLHF----PFLSSFWVLTBEAWQ 1035

Qy 287 KFWRSQAQMPPN-IEKNPSRVG---TLVVLISITIL---YAGINFSCMWSALQLRADR 337  
Db 1036 SYMAYTGHLRURLIRKRFCLGWLGLPAWVAISVGFTKAKGYSTNNY-CWLSL----- 1087

Qy 338 DLVIDKCONWGNGHLHYSVRLVENVIMVLVPEFGVK-----VILANYC--HS 381

Db 1088 ---EGGLLYAPFGPAAAVVLMVIGLIVFNKLVSQDGITDKKKLKERAGASLWSSCVLP 1144

Qy 382 LIAAQJIAVJLISIDEMILLFOYLHPLRSLEPTHNVVDYLHCV 423  
Db 1145 LLALTMSAVLAVTDRRSALQILFAVFDSDLEGFTVVMVHCl 1186

Search completed: April 1, 2003, 08:49:02  
Job time : 52 sec